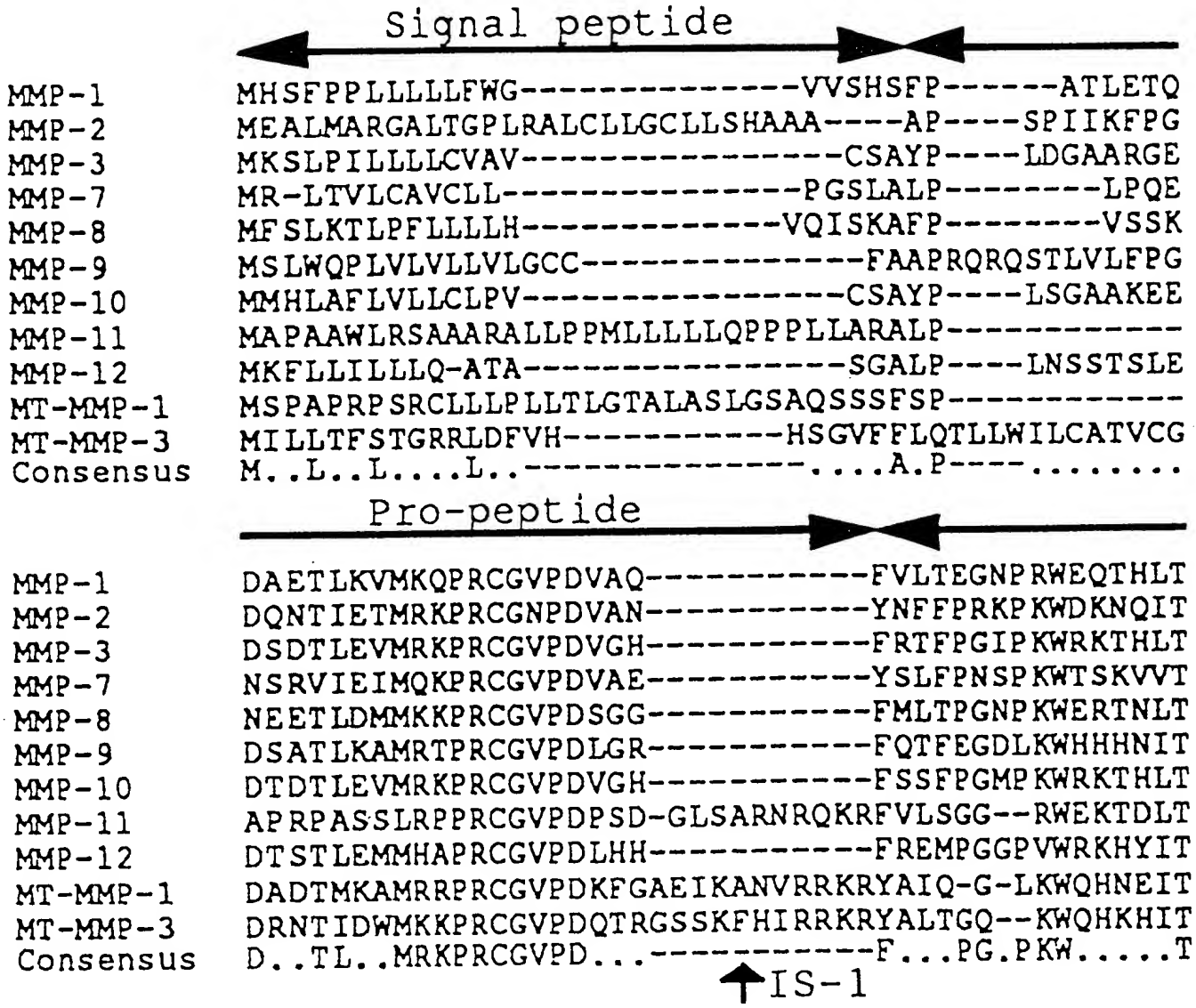
09734760 "2002/12/27

FIG. 1A-1



002727 "200nE260

FIG. IA-2

Pro-peptide

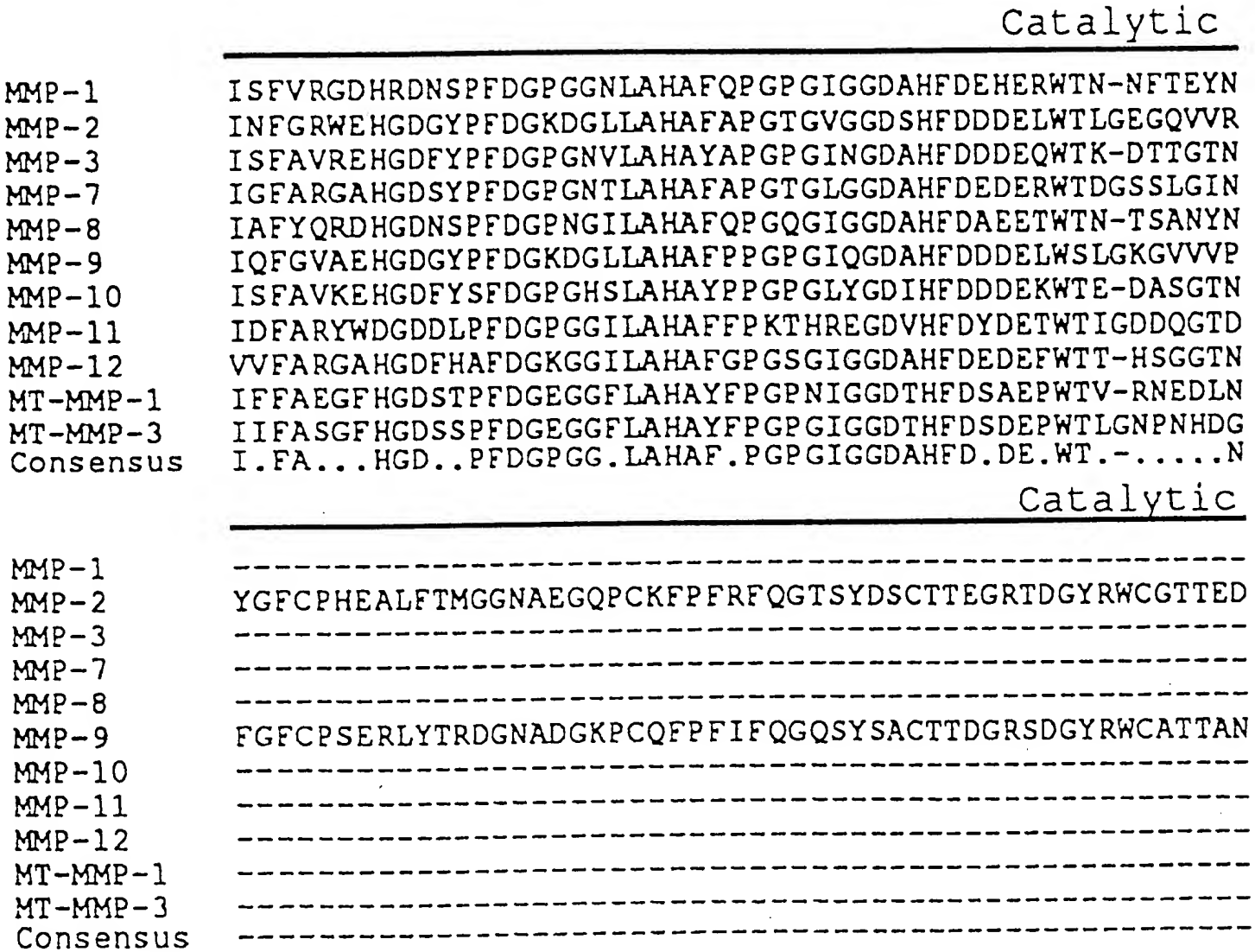
```
EQDVDLVQKYLEKYYNLKNDGRQVEKRRNSGPVV-EKLKQMQEFFGLKVTGKP    79
DVAPK-TDKELAVQYLNTF-YGCPKE-SCNLFVLKDTLKKMQKFFGLPQTGDL    89
DTSMNLVQKYLENYYDLKKDVKQFVRRKDSGPVV-KKIREMQKFLGLEVTGKL    79
AGGMSELQWEQAQDY-LKRFYLYDSETKNANSLE-AKLKEMQKFFGLPITGML    74
EKNTKTVQDYLEKFYQLPSNQYQSTR-KNGTNVIVEKLKEMQRFFGLNVTGKP    78
DLRTNLTDRQLAEEYLYRYGYTRVAEMRGESKSLGPALLLLQKQLSLPETGEL    86
DSNKDLAQQYLEKYYNLEKDVKQFRRK-DSNLIV-KKIQGMQKFLGLEVTGKL    78
-----------PDVHHLHAERRGPQ----------PWHAALPSSPAPAPATQE    67
KNNVLFGERYLEKFYGLEINKLPVTKMKYSGNLMKEKIQEMQHFLGLKVTGQL    79
-------EAWLQQYGYLPPGDLRTHTQRSPQSLS-AAIAAMQKFYGLQVTGKA    80
TEQYFNVEVWLQKYGYLPPTSPRMSVVRSAETMQ-SALAAMQQFYGINMTGKV    88
.........L...Y.L.................-.KL..MQKF.GL.VTGKL   100
```

Catalytic

```
YRIENYTPDLPRADVDHAIEKAFQLWSNVTPLTFTKV--------SEGQADIM   160
YRIIGYTPDLDPETVDDAFARAFQVWSDVTPLRFSRI--------HDGEADIM   170
YRIVNYTPDLPKDAVDSAVEKALKVWEEVTPLTFSRL--------YEGEADIM   160
YRIVSYTRDLPHITVDRLVSKALNMWGKEIPLHFRKV--------VWGTADIM   155
YRIRNYTPQLSEAEVERAIKDAFELWSVASPLIFTRI--------SQGEADIN   159
YWIQNYSEDLPRAVIDDAFARAFALWSAVTPLTFTRV--------YSRDADIV   167
YRIVNYTPDLPRDAVDSAIEKALKVWEEVTPLTFSRL--------YEGEADIM   159
YRILRFPWQLVQEQVRQTMAEALKVWSDVTPLTFTEV--------HEGRADIM   156
YRINNYTPDMNREDVDYAIRKAFQVWSNVTPLKFSKI--------NTGMADIL   160
FCIQNYTPKVGEYATYEAIRKAFRVWESATPLRFREVPYAYIREGHEKQADIM   178
YSIKNVTPKVGDPETRKAIRRAFDVWQNVTPLTFEEVPYSELENGK-RDVDIP   185
YRI.NYTPDL....VD.AI.KAF.VWS.VTPLTF..V--------..G.ADIM   200
                                    ↑IS-2
```

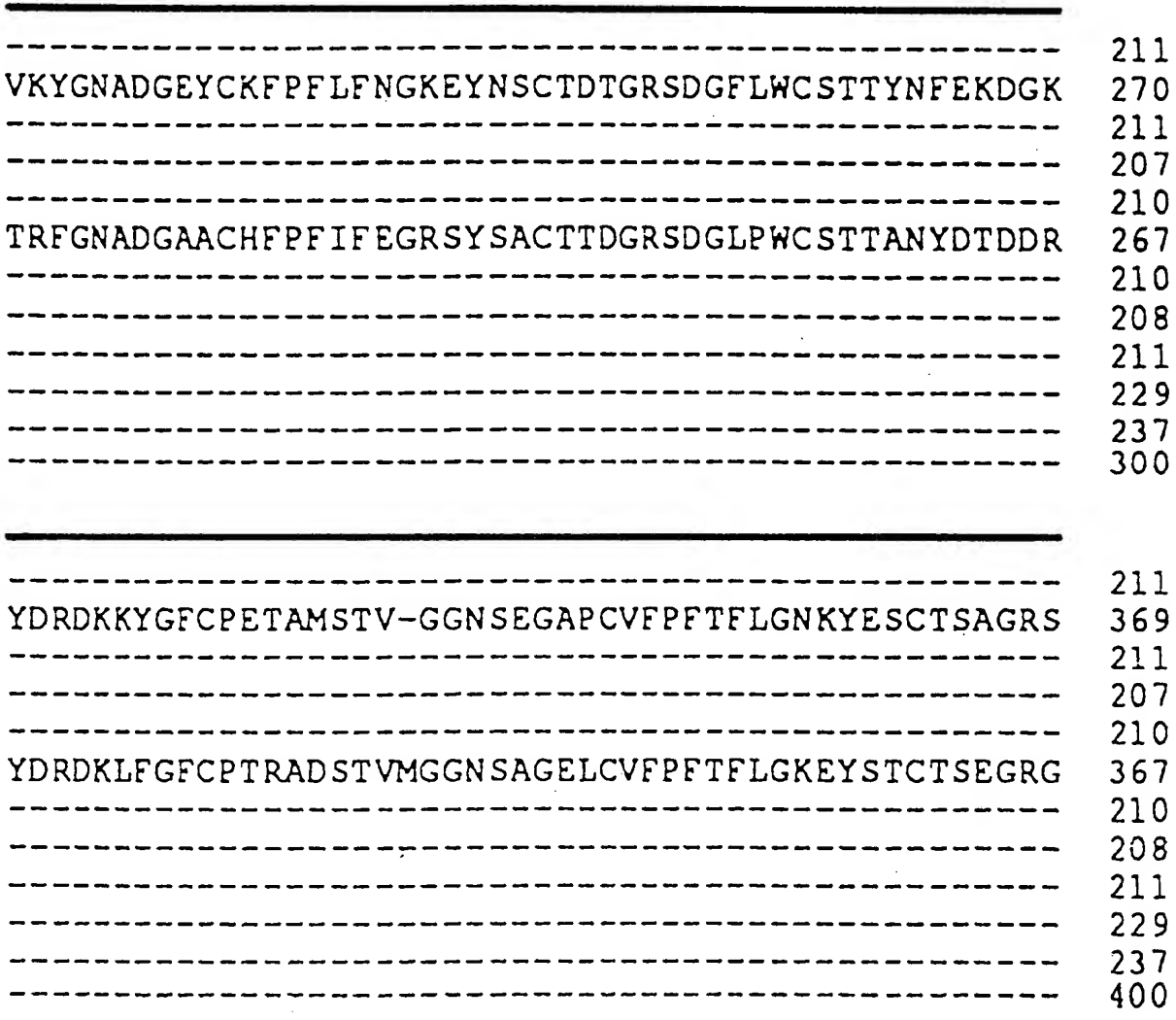
09734760 "20021"

FIG. IB-1



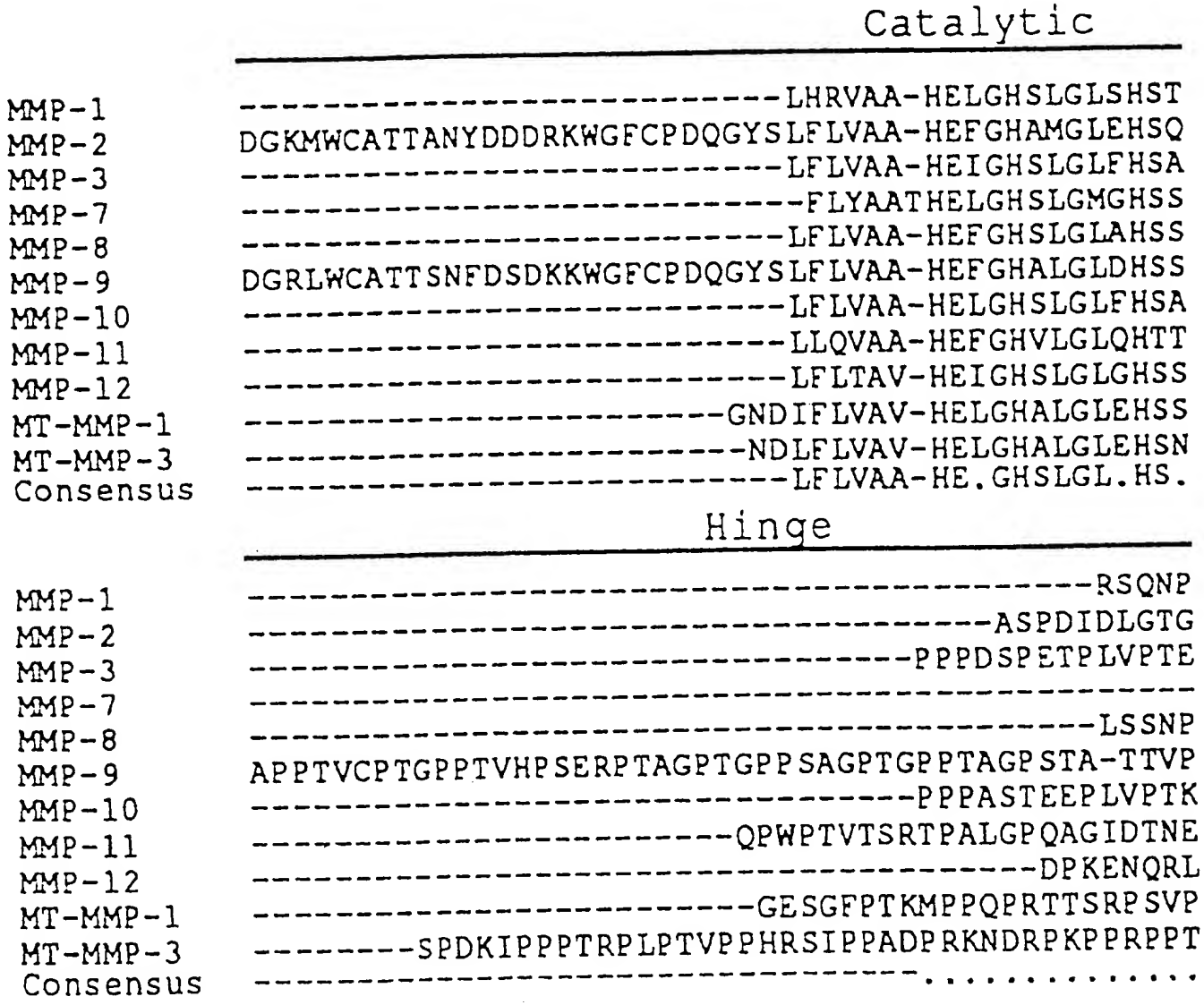
002727 "200n8260

FIG. 1B-2



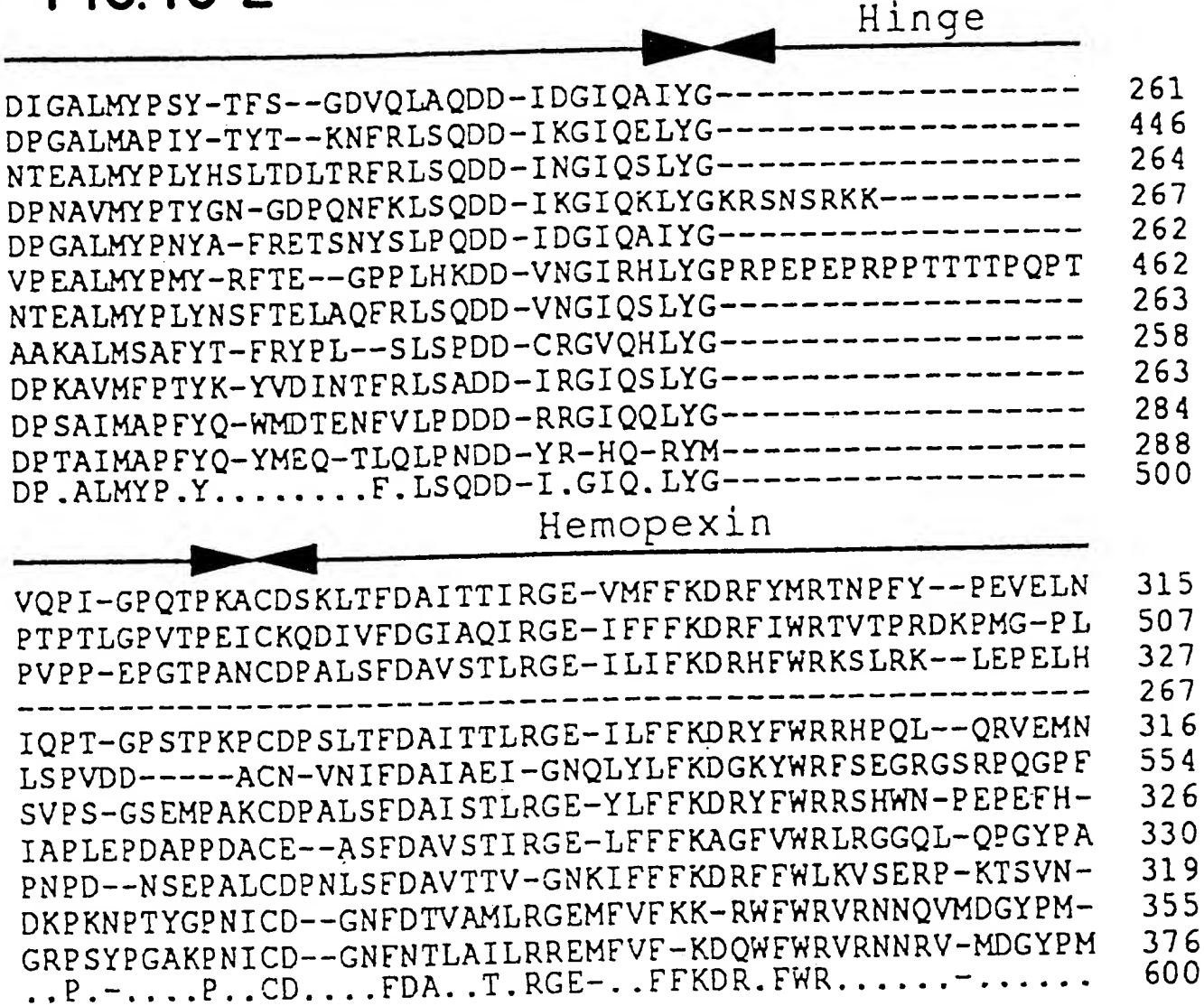
0027217 200h760

FIG. IC-1



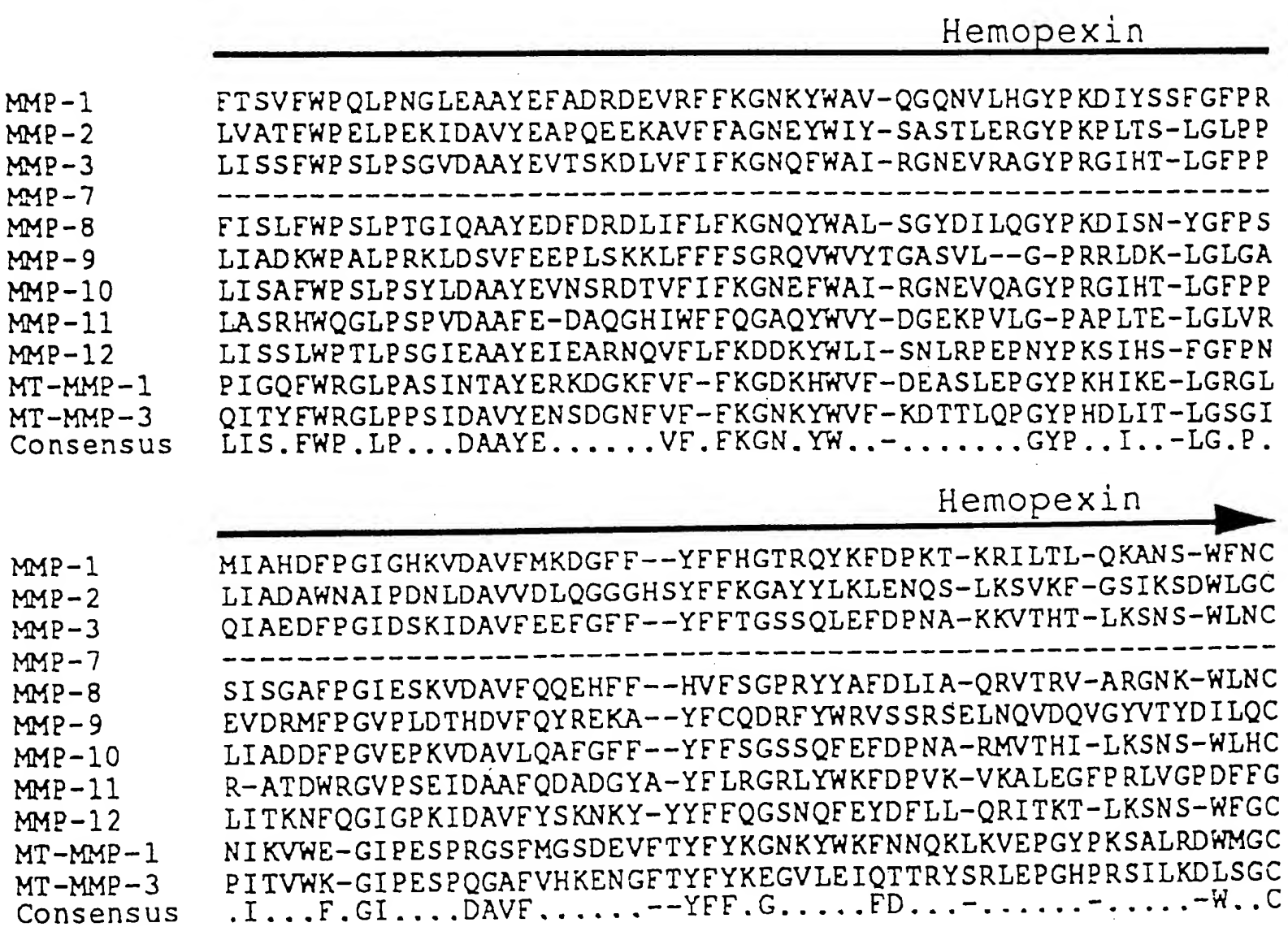
09/760,827 Filed 01/12/2001

FIG. 1C-2



0027217 200E760

FIG. ID-1



09234260 "27270

FIG. ID-2

```
TVKHIDAA-LSEENTGKTYFFVANKYWRYDEYKRSMDPGYPK   413
DVQRVDAA-FNWSKNKKTYIFAGDKFWRYNEVKKKMDPGFPK   604
TVRKIDAA-ISDKEKNKTYFFVEDKYWRFDEKRNSMEPGFPK   424
-------------------------------------------  267
SVQAIDAA-VFYRS--KTYFFVNDQFWRYDNQRQFMEPGYPK   411
DVAQVTGA-LRSGR-GKMLLFSGRRLWRFDVKAQMVDPRSAS   648
TIRKIDAA-VSDKEKKKTYFFAADKYWRFDENSQSMEQGFPR   423
FP--VHAALVWGPEKNKIYFFRGRDYWRFHPSTRRVDSPVPR   424
FVKKIDAA-VFNPRFYRTYFFVDNQYWRYDERRQMMDPGYPK   416
PTDKIDAA-LFWMPNGKTYFFRGNKYYRFNEELRAVDSEYPK   451
PPHGIDSA-IWWEDVGKTYFFKGDRYWRYSEEMKTMDPGYPK   472
.V..IDAA-.......KTYFF....YWR.DE....MDPG.PK   700


RKN------------------------------------------  469
-------------------------------------------  660
-------------------------------------------  477
-------------------------------------------  267
RYG------------------------------------------  467
PED------------------------------------------  707
-------------------------------------------  476
CAEPANTFL------------------------------------  488
-------------------------------------------  470
PSGGRPDEGTEEETE-VIIIEVDEEGGGAVSAAAVVLPVLLL   549
DGPTDRVKEGHSPPDDVDIVIKLDNTASTVKAIAIVIPCILA   571
-------------------------------------------  800
```

IS-3

09/540,126 03/31/2000

FIG. 1E

MMP-1	----------	469
MMP-2	----------	660
MMP-3	----------	477
MMP-7	----------	267
MMP-8	----------	468
MMP-9	----------	708
MMP-10	----------	476
MMP-11	----------	489
MMP-12	----------	470
MT-MMP-1	LLVLAVGLAVFFFRRHGTPRRLLYCQRSLLDKV	582
MT-MMP-3	LCLLVLVYTVFQFKRKGTPRHILYCKRSMQEWV	604
Consensus	----------	833

09734060 "12200

FIG. 2

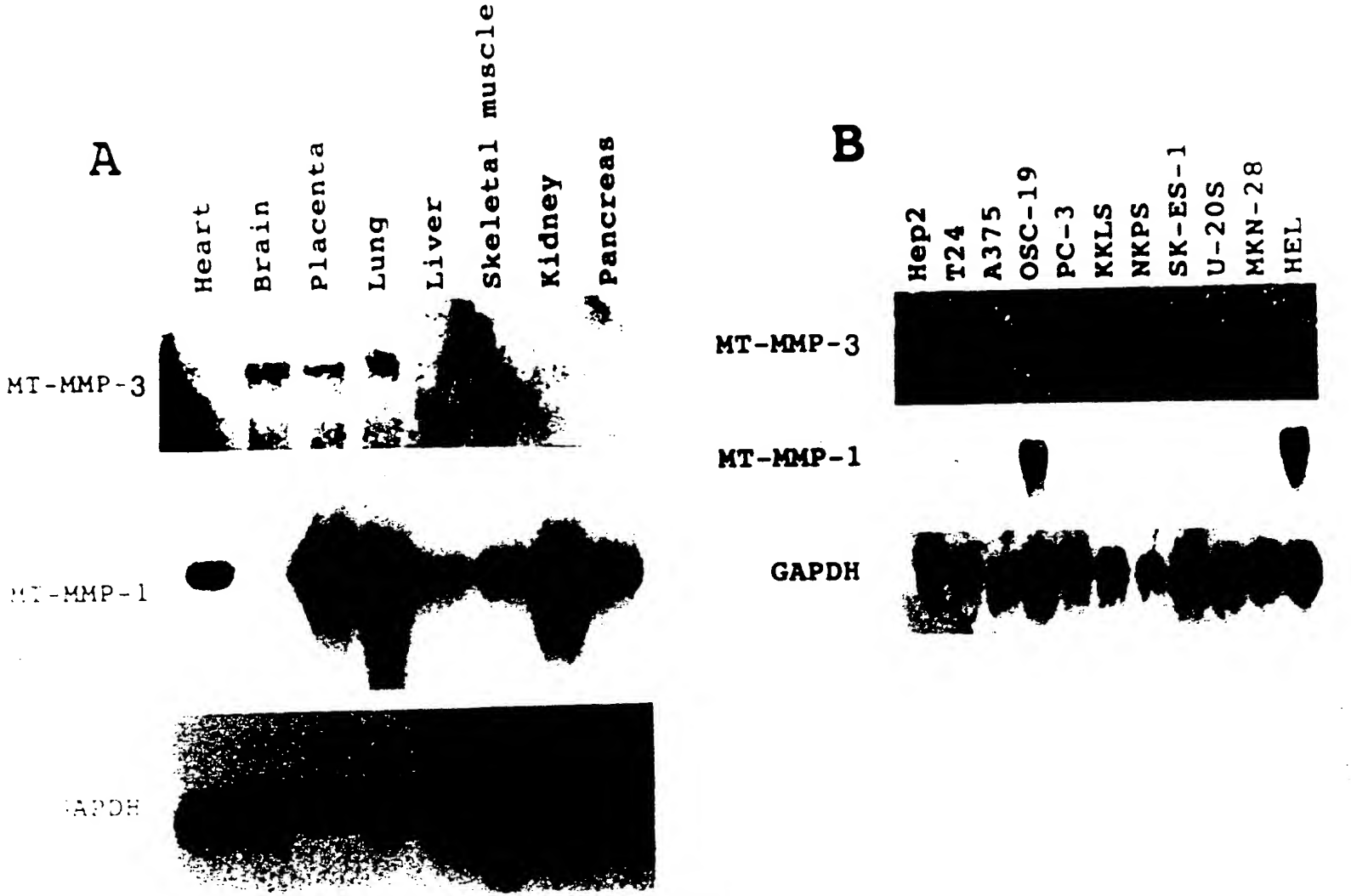


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FIG. 3

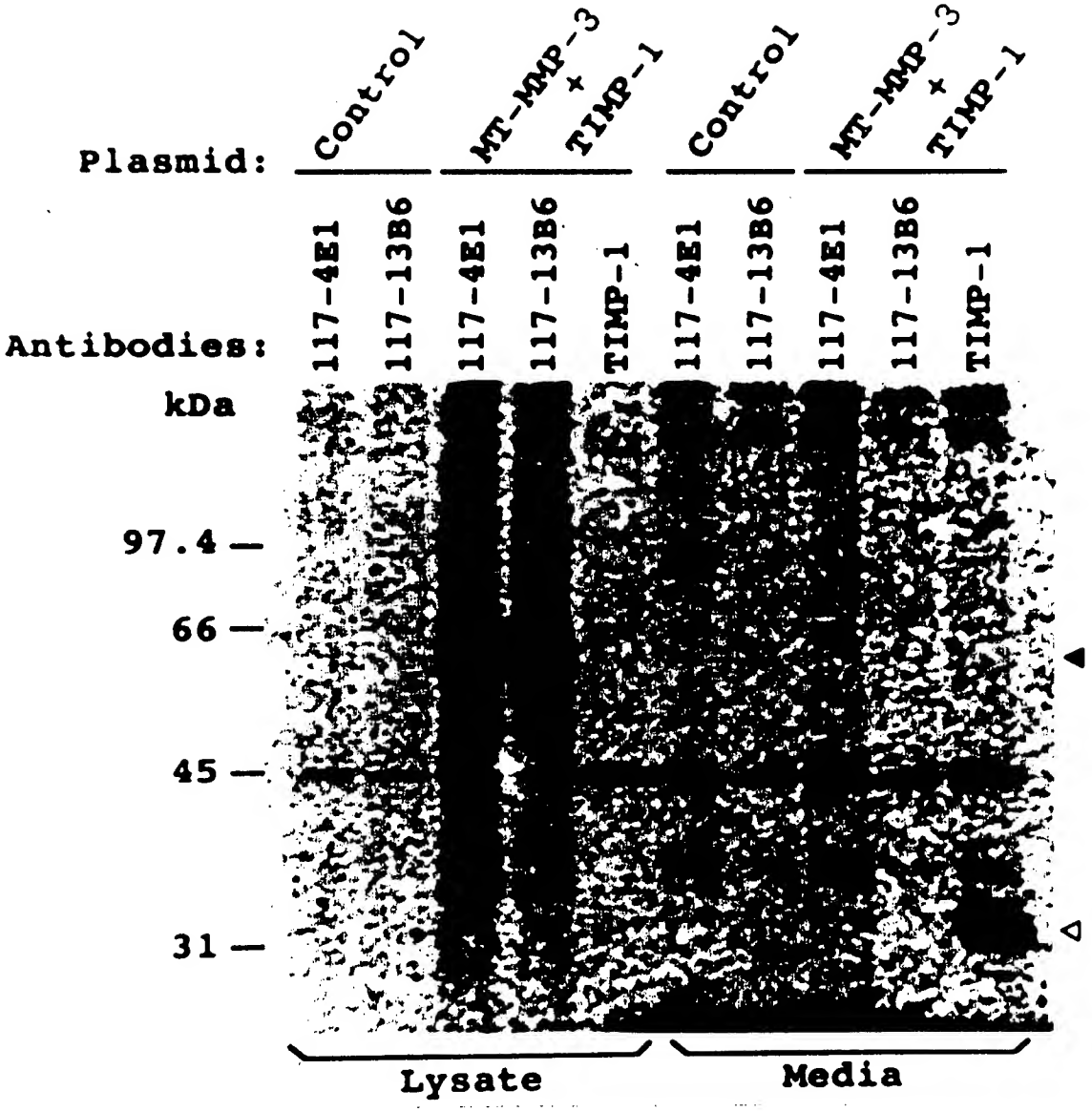

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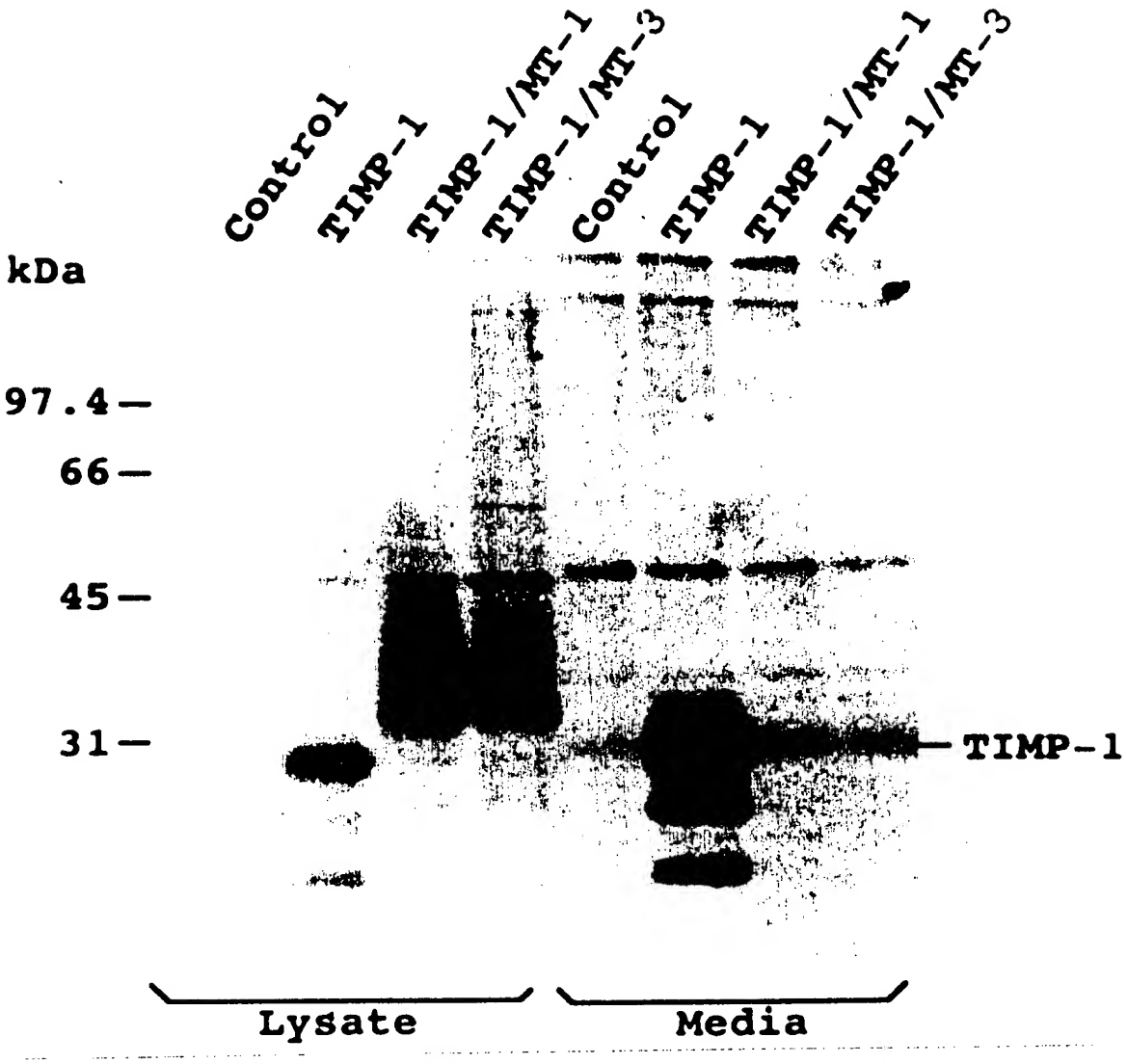
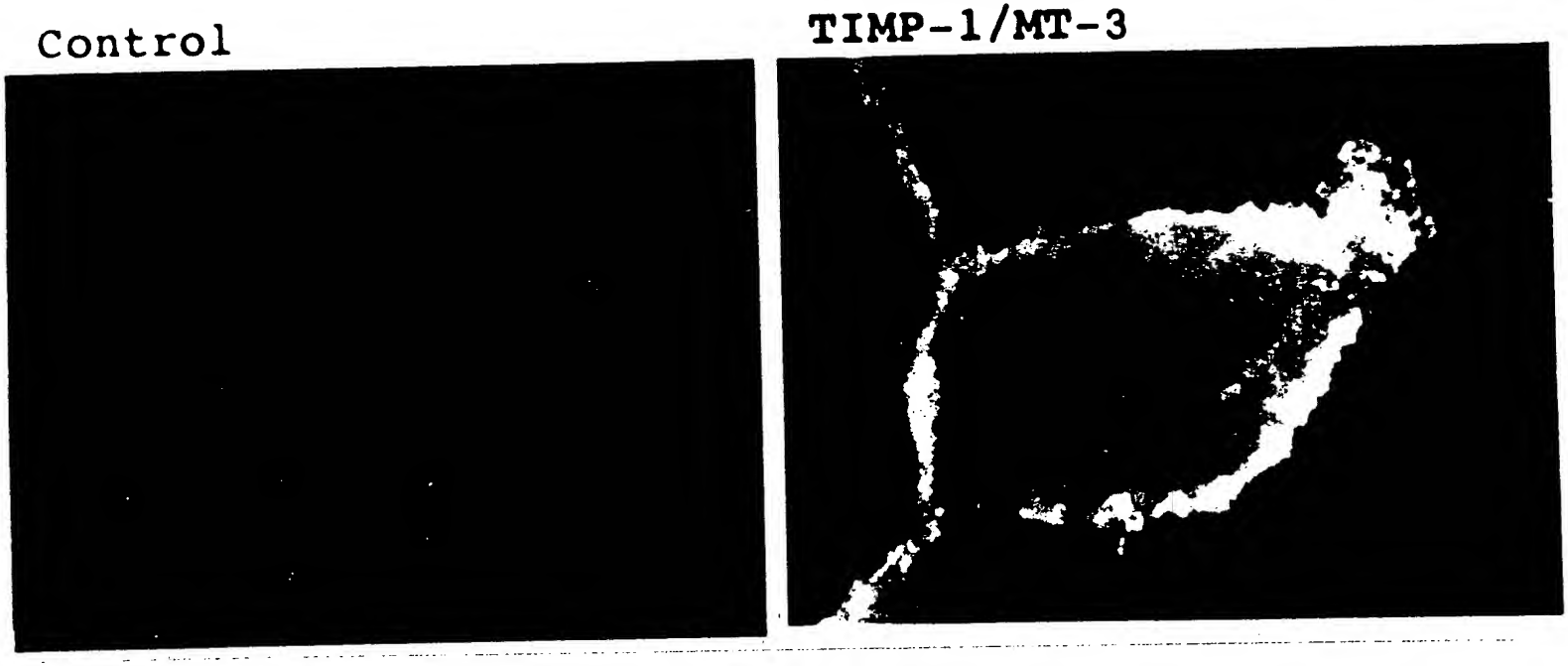
FIG. 4



00212F "200HE260

FIG. 5



09734760 "20041207"

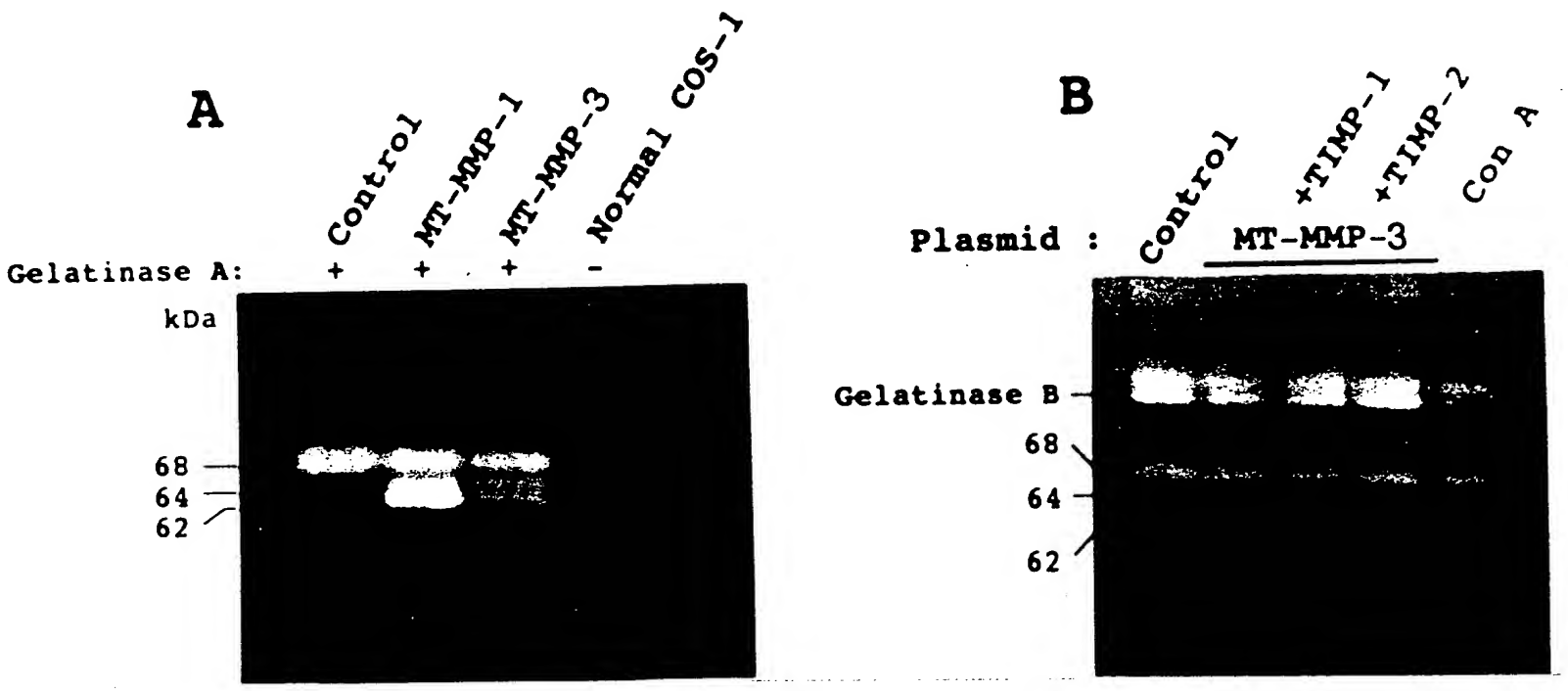



FIG. 6